WEST Search History

| Hide Items | Restore | Clear | Cancel |

DATE: Monday, March 28, 2005

| Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ	
☐	L13	l3 and l9	0
☐	L12	l9 and L11	0
☐	L11	l7.ab.	400
☐	L10	L9 and l7	28
☐	L9	(536/23.1)![CCLS]	11636
☐	L8	L7 and l1	1
☐	L7	aldose reducta$	1684
☐	L6	aldose reducta?	1
☐	L5	TTGTGGCCCACTTCCAGATCGAGAAGCTCT	0
☐	L4	L3 and l1	1
☐	L3	L2.ab.	48
☐	L2	ARL	1090
☐	L1	dai.in.	2665

END OF SEARCH HISTORY

```
      FILE 'MEDLINE' ENTERED AT 13:43:08 ON 28 MAR 2005
L1            0 S DAI/AU
L2         2321 S ALDOSE REDUCTASE
L3          312 S ARL
L4         2625 S L2 OR L3
L5            0 S TTGTGGCCCACTTCCAGATCGAGAAGCTCT

      FILE 'PCTFULL' ENTERED AT 13:43:59 ON 28 MAR 2005
L6            0 S TTGTGGCCCACTTCCAGATCGAGAAGCTCT
L7          420 S DAI/AU
L8          602 S ALDOSE REDUCTASE
L9            0 S L8 AND L7
L10        6141 S ARL
L11           3 S L10 AND L7
```
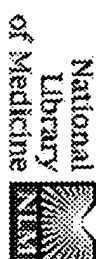
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National Library of Medicine

Search [PubMed ▼] for [#5 AND #1] [Preview] [Go] [Clear]

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Text Version

Field: Title/Abstract

- Search History will be lost after eight hours of inactivity.
- To combine searches use # before search number, e.g., #2 AND #6.
- Search numbers may not be continuous; all searches are represented.
- Click on query # to add to strategy

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NLM Catalog
NLM Gateway
TOXNET
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ClinicalTrials.gov
PubMed Central

Search   **Most Recent Queries**   **Time**   **Result**

#6   Search #5 AND #1 Field: Title/Abstract   13:41:18   1
#5   Search #4 OR #3 Field: Title/Abstract   13:41:06   2616
#4   Search ARL Field: Title/Abstract   13:40:51   290
#3   Search aldose reductase Field: Title/Abstract   13:40:33   2334
#2   Search aldose reductase Field: Author   13:40:24   0
#1   Search dai Field: Author   13:40:12   4793

[Clear History]

```
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OM nucleic - nucleic search, using sw model
                     ,
Run on:           March 22, 2005, 22:07:10 ; Search time 4250 Seconds
                                            (without alignments)
                                            9762.366 Million cell updates/sec


Title:            US-10-653-681A-1
Perfect score:    1090
Sequence:         1 caaaaacagcaacagaaagc..........ataaaaaaaataataatcat 1090


Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0


Searched:         34239544 seqs, 19032134700 residues


Total number of hits satisfying chosen parameters:      68479088


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :        EST:*
                  1:  gb_est1:*
                  2:  gb_est2:*
                  3:  gb_htc:*
                  4:  gb_est3:*
                  5:  gb_est4:*
                  6:  gb_est5:*
                  7:  gb_est6:*
                  8:  gb_gss1:*
                  9:  gb_gss2:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                 SUMMARIES
                          %
Result                    Query
    No.    Score   Match Length DB   ID                     Description
--------------------------------------------------------------------------------
 c   1    705.4    64.7    735   5   BM981698               BM981698 UI-CF-EN1
     2    685.2    62.9   1586   3   CR607509               CR607509 full-leng
 c   3     666     61.1    746   2   BF688991               BF688991 602185236
 c   4    652.2    59.8    796   5   BX337598               BX337598 BX337598
     5     647     59.4    909   4   BG169378               BG169378 602320937
 c   6    586.6    53.8    666   1   AI924753               AI924753 wn58a02.x
     7     585     53.7    613   6   CB132708               CB132708 K-EST0183
 c   8     573     52.6    595   5   BM983180               BM983180 UI-CF-EN1
```

c	9	570.8	52.4	593	5	BU677104	BU677104 UI-CF-DU1
	10	542.4	49.8	623	4	BM793014	BM793014 K-EST0073
	11	526.2	48.3	969	7	CO581979	CO581979 ILLUMIGEN
	12	522	47.9	1012	5	BQ943650	BQ943650 AGENCOURT
c	13	521.6	47.9	540	1	AA804597	AA804597 nk97e06.s
c	14	518.2	47.5	644	6	CA450136	CA450136 UI-CF-FN0
	15	517	47.4	588	2	BE785963	BE785963 601478213
	16	506.8	46.5	881	7	CO580792	CO580792 ILLUMIGEN
	17	502.6	46.1	704	7	CO582646	CO582646 ILLUMIGEN
	18	498.8	45.8	620	6	CB118695	CB118695 K-EST0165
	19	481.4	44.2	635	7	CV334625	CV334625 IL3-UT011
c	20	475.4	43.6	496	2	AW379341	AW379341 MR0-HT024
c	21	460	42.2	920	2	BE964368	BE964368 601658069
	22	456.4	41.9	592	4	BM819663	BM819663 K-EST0087
	23	449.4	41.2	786	5	BQ221381	BQ221381 AGENCOURT
c	24	447.2	41.0	452	1	AI393702	AI393702 tg66d01.x
c	25	446.4	41.0	456	1	AI292337	AI292337 qm77c02.x
c	26	446.4	41.0	458	1	AI744504	AI744504 wg09a09.x
c	27	446.4	41.0	460	1	AI291463	AI291463 qm73h04.x
	28	446.4	41.0	582	5	BP278752	BP278752 BP278752
c	29	432	39.6	446	5	BX104876	BX104876 BX104876
c	30	426.6	39.1	445	1	AI301329	AI301329 qn27e09.x
	31	426.4	39.1	914	7	CO775128	CO775128 ILLUMIGEN
c	32	426	39.1	448	5	BM975664	BM975664 UI-CF-EN1
	33	417	38.3	445	6	CB161124	CB161124 K-EST0220
	34	402.4	36.9	581	5	BP263763	BP263763 BP263763
c	35	392.6	36.0	415	1	AA947514	AA947514 oq53h01.s
	36	388.8	35.7	453	4	BG197874	BG197874 RST17122
	37	384.8	35.3	912	5	BQ220848	BQ220848 AGENCOURT
c	38	383.4	35.2	405	6	C75075	C75075 C75075 Huma
c	39	378	34.7	388	1	AI831519	AI831519 wj49h11.x
	40	373	34.2	384	2	BE787870	BE787870 601479812
c	41	370.6	34.0	386	1	AI813308	AI813308 wj33c01.x
c	42	365.2	33.5	388	2	BE711936	BE711936 QV2-HT069
	43	360	33.0	796	4	BG682196	BG682196 602629503
	44	351.2	32.2	1342	3	AK075865	AK075865 Mus muscu
	45	348	31.9	1236	3	AK019906	AK019906 Mus muscu

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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 19, 2005, 00:09:26 ; Search time 40.5 Seconds
                                            (without alignments)
                                            4018.147 Million cell updates/sec

Title: US-10-653-681A-1
Perfect score: 1928
Sequence: 1 caaaaacagcaacagaaagc..........ataaaaaaaataataatcat 1090

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10653681/runat_18032005_171051_1302/app_query.fasta_1.128
7
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10653681_@CGN_1_1_46_@runat_18032005_171051_1302 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES

Result NO.	Score	% Query Match	Length	DB	ID	Description
1	1265	65.6	356	4	US-09-949-016-7215	Sequence 7215, Ap

```
                            us-10-653-681a-1:n2p.rai
2     1154   59.9    316  4  US-09-702-705-340       Sequence 340, App
3     1154   59.9    316  4  US-09-736-457-340       Sequence 340, App
4     1154   59.9    316  4  US-09-614-124B-340      Sequence 340, App
5     1154   59.9    316  4  US-09-671-325-340       Sequence 340, App
6     1154   59.9    316  4  US-09-589-184-340       Sequence 340, App
7     1154   59.9    316  4  US-09-658-824-340       Sequence 340, App
8      889   46.1    316  3  US-08-801-344-4         Sequence 4, Appli
9      889   46.1    316  3  US-09-498-599-4         Sequence 4, Appli
10     877   45.5    316  1  US-08-585-595-3         Sequence 3, Appli
11     612   31.7    302  4  US-09-270-767-45294     Sequence 45294, A
12   586.5   30.4    326  4  US-09-949-016-6679      Sequence 6679, Ap
13   585.5   30.4    347  4  US-09-949-016-11456     Sequence 11456, A
14     532   27.6    323  4  US-09-949-016-6133      Sequence 6133, Ap
15     530   27.5    325  4  US-09-949-016-7170      Sequence 7170, Ap
16     526   27.3    323  4  US-09-702-705-1821      Sequence 1821, Ap
17     526   27.3    323  4  US-09-736-457-1821      Sequence 1821, Ap
18     526   27.3    323  4  US-09-671-325-1821      Sequence 1821, Ap
19     516   26.8    323  3  US-08-532-896-2         Sequence 2, Appli
20     514   26.7    364  4  US-09-643-597-172       Sequence 172, App
21     514   26.7    364  4  US-09-480-884A-172      Sequence 172, App
22     514   26.7    364  4  US-09-702-705-783       Sequence 783, App
23     514   26.7    364  4  US-09-736-457-783       Sequence 783, App
24     514   26.7    364  4  US-09-542-615A-172      Sequence 172, App
25     514   26.7    364  4  US-09-606-421B-172      Sequence 172, App
26     514   26.7    364  4  US-09-614-124B-783      Sequence 783, App
27     514   26.7    364  4  US-09-671-325-783       Sequence 783, App
28     514   26.7    364  4  US-09-589-184-783       Sequence 783, App
29     514   26.7    364  4  US-09-466-396A-172      Sequence 172, App
30     514   26.7    364  4  US-09-476-496A-172      Sequence 172, App
31     514   26.7    364  4  US-09-630-940B-172      Sequence 172, App
32     514   26.7    364  4  US-09-658-824-783       Sequence 783, App
33     514   26.7    364  4  US-09-285-479-172       Sequence 172, App
34     485   25.2    297  4  US-09-949-016-9693      Sequence 9693, Ap
35     473   24.5    323  3  US-08-853-839-2         Sequence 2, Appli
36     459   23.8    283  4  US-09-949-016-7078      Sequence 7078, Ap
37     438   22.7    309  3  US-09-166-412-2         Sequence 2, Appli
38     438   22.7    309  3  US-09-347-803-26        Sequence 26, Appl
39     438   22.7    309  4  US-08-731-320B-2        Sequence 2, Appli
40     438   22.7    309  4  US-09-166-438-2         Sequence 2, Appli
41   435.5   22.6    346  4  US-09-270-767-46713     Sequence 46713, A
42   424.5   22.0    309  3  US-09-347-803-14        Sequence 14, Appl
43   411.5   21.3    308  3  US-09-347-803-12        Sequence 12, Appl
44     402   20.9    308  3  US-09-347-803-10        Sequence 10, Appl
45   400.5   20.8    326  4  US-09-270-767-43738     Sequence 43738, A
```

us-10-653-681a-1.n2p.rapb

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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 19, 2005, 00:25:42 ; Search time 162 Seconds
                                           (without alignments)
                                           4448.023 Million cell updates/sec

Title: US-10-653-681A-1
Perfect score: 1928
Sequence: 1 caaaaacagcaacagaaagc..........ataaaaaaaataataatcat 1090

Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop 6.0 , Fgapext 7.0
                Delop   6.0 , Delext   7.0

Searched: 1401741 seqs, 330541175 residues

Total number of hits satisfying chosen parameters: 2803482

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10653681/runat_18032005_171053_1387/app_query.fasta_1.128
7
-DB=Published_Applications_AA -QFMT=fastan -SUFFIX=n2p.rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10653681_@CGN_1_1_199_@runat_18032005_171053_1387
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_AA:*
                1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
                10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
                11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
                12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
                17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

```
18:  /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19:  /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20:  /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1268	65.8	358	9	US-09-925-299-923	Sequence 923, App
2	1268	65.8	358	10	US-09-925-299-923	Sequence 923, App
3	1159	60.1	316	14	US-10-274-375-3	Sequence 3, Appli
4	1154	59.9	316	9	US-09-736-457-340	Sequence 340, App
5	1154	59.9	316	9	US-09-902-941-340	Sequence 340, App
6	1154	59.9	316	9	US-09-849-626-340	Sequence 340, App
7	1154	59.9	316	10	US-09-476-300-340	Sequence 340, App
8	1154	59.9	316	14	US-10-017-754-340	Sequence 340, App
9	1154	59.9	316	14	US-10-113-872-340	Sequence 340, App
10	1154	59.9	316	15	US-10-283-017-340	Sequence 340, App
11	1073	55.7	316	14	US-10-274-375-2	Sequence 2, Appli
12	1058	54.9	316	14	US-10-274-694-18	Sequence 18, Appl
13	889	46.1	316	15	US-10-205-331-28	Sequence 28, Appl
14	879	45.6	316	16	US-10-451-861-30	Sequence 30, Appl
15	876	45.4	315	16	US-10-826-679-1	Sequence 1, Appli
16	875	45.4	316	16	US-10-408-765A-1573	Sequence 1573, Ap
17	875	45.4	316	16	US-10-416-330-43	Sequence 43, Appl
18	784	40.7	318	15	US-10-258-080-10	Sequence 10, Appl
19	774	40.1	245	17	US-10-653-681A-4	Sequence 4, Appli
20	638.5	33.1	176	16	US-10-451-861-31	Sequence 31, Appl
21	622	32.3	301	14	US-10-321-204-51	Sequence 51, Appl
22	613.5	31.8	302	15	US-10-038-854-44	Sequence 44, Appl
23	586.5	30.4	326	15	US-10-161-927-88	Sequence 88, Appl
24	583.5	30.3	279	15	US-10-038-854-398	Sequence 398, App
25	582.5	30.2	307	14	US-10-354-358-122	Sequence 122, App
26	579.5	30.1	269	15	US-10-038-854-52	Sequence 52, Appl
27	571	29.6	325	16	US-10-472-317-36	Sequence 36, Appl
28	560	29.0	325	14	US-10-354-358-114	Sequence 114, App
29	560	29.0	353	9	US-09-925-301-1181	Sequence 1181, Ap
30	560	29.0	353	14	US-10-106-698-4568	Sequence 4568, Ap
31	557.5	28.9	304	14	US-10-274-694-4	Sequence 4, Appli
32	554	28.7	323	14	US-10-321-204-30	Sequence 30, Appl
33	540	28.0	323	15	US-10-038-854-14	Sequence 14, Appl
34	539	28.0	323	14	US-10-177-293-4	Sequence 4, Appli
35	539	28.0	323	14	US-10-321-204-1	Sequence 1, Appli
36	539	28.0	323	15	US-10-038-854-124	Sequence 124, App
37	539	28.0	323	15	US-10-403-161-78	Sequence 78, Appl
38	539	28.0	323	15	US-10-403-161-94	Sequence 94, Appl
39	539	28.0	337	15	US-10-403-161-90	Sequence 90, Appl
40	537	27.9	326	16	US-10-476-033-2	Sequence 2, Appli
41	536	27.8	323	14	US-10-321-204-7	Sequence 7, Appli
42	536	27.8	323	15	US-10-038-854-122	Sequence 122, App
43	536	27.8	323	15	US-10-403-161-86	Sequence 86, Appl
44	536	27.8	323	15	US-10-403-161-92	Sequence 92, Appl
45	534	27.7	323	15	US-10-403-161-82	Sequence 82, Appl

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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 19, 2005, 00:08:46 ; Search time 49.5 Seconds
                                            (without alignments)
                                            4237.425 Million cell updates/sec

Title: US-10-653-681A-1
Perfect score: 1928
Sequence: 1 caaaaacagcaacagaaagc..........ataaaaaaataataatcat 1090

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10653681/runat_18032005_171051_1290/app_query.fasta_1.
1287
-DB=PIR_79 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10653681_@CGN_1_1_63_@runat_18032005_171051_1290 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   PIR_79:*
                  1: pir1:*
                  2: pir2:*
                  3: pir3:*
                  4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1017	52.7	316	2	A53440	aldose reductase h
2	961	49.8	316	2	A37990	aldose reductase h
3	889	46.1	316	1	A60603	aldehyde reductase
4	879	45.6	316	2	I49484	aldehyde reductase
5	877	45.5	315	1	A35452	aldehyde reductase
6	875	45.4	316	1	A39763	aldehyde reductase
7	870	45.1	302	2	A34406	aldehyde reductase
8	870	45.1	316	2	A59021	aldehyde reductase
9	586.5	30.4	326	1	S41120	cholestenone 5beta
10	571	29.6	325	1	JN0629	alcohol dehydrogen
11	564.5	29.3	326	1	S15835	3-oxo-5beta-steroi
12	560	29.0	325	2	A33851	alcohol dehydrogen
13	554	28.7	323	1	A45366	20alpha-hydroxyste
14	539	28.0	323	2	A53436	3-alpha-hydroxyste
15	536	27.8	323	2	JC5240	3alpha-hydroxychol
16	532	27.6	323	1	A57407	chlordecone reduct
17	527	27.3	323	1	JH0575	prostaglandin-F sy
18	524	27.2	323	1	A28396	prostaglandin-F sy
19	522	27.1	323	2	I73676	chlordecone reduct
20	517	26.8	329	2	I53872	dihydrodiol dehydr
21	516	26.8	320	2	I73675	chlordecone reduct
22	514	26.7	324	1	JC4280	carbonyl reductase
23	510	26.5	323	2	I73674	chlordecone reduct
24	509	26.4	323	1	A56424	estradiol 17beta-d
25	508	26.3	323	2	B57407	3alpha-hydroxyster
26	491	25.5	316	2	T26766	hypothetical prote
27	474	24.6	323	1	JC2330	luteal 20-alpha-hy
28	471.5	24.5	322	1	A39350	3alpha-hydroxyster
29	451	23.4	309	2	A84599	hypothetical prote
30	449.5	23.3	309	2	B84599	hypothetical prote
31	433.5	22.5	327	1	S76143	probable aldehyde
32	418	21.7	290	2	T02543	aldehyde dehydroge
33	398	20.6	496	2	B89027	protein T08H10.1 [
34	396.5	20.6	284	1	A32950	probable aldehyde
35	389	20.2	310	2	T17013	D-sorbitol-6-phosp
36	386	20.0	313	2	T09670	abscisic acid acti
37	384.5	19.9	317	2	T25526	hypothetical prote
38	380	19.7	274	2	AC1535	oxydoreductases ho
39	379.5	19.7	225	1	CYFGE	epsilon-crystallin
40	377	19.6	277	2	D89964	hypothetical prote
41	377	19.6	312	1	S22846	probable aldehyde
42	374	19.4	252	2	S61515	dihydrodiol dehydr
43	373	19.3	274	2	AG1177	oxydoreductases ho
44	370	19.2	350	2	B84797	probable alcohol d
45	368.5	19.1	280	2	D69988	plant metabolite d

us-10-653-681a-1.n2p.rup

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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 19, 2005, 00:08:07 ; Search time 220.5 Seconds
                                            (without alignments)
                                            5062.733 Million cell updates/sec

Title: US-10-653-681A-1
Perfect score: 1928
Sequence: 1 caaaaacagcaacagaaagc.........ataaaaaaaataataatcat 1090

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10653681/runat_18032005_171050_1279/app_query.fasta_1.128
7
-DB=UniProt_03 -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10653681_@CGN_1_1_244_@runat_18032005_171050_1279 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   UniProt_03:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                       %
Result   Query
   No.   Score Match Length DB ID   Description
       ----
        1   1159   60.1   316 1 AKBA_HUMAN   O60218 homo sapien
        2   1149   59.6   316 2 Q8IWZ1   Q8iwz1 homo sapien
        3   1029   53.4   315 1 ALD2_CRIGR   O08782 cricetulus
        4   1013   52.5   315 1 ALD2_MOUSE   P45377 mus musculu
        5   1001   51.9   316 2 Q91W30   Q91w30 rattus norv

                                    Page 1

6	992	51.5	316	2	Q8BIV6	Q8biv6 mus musculu
7	990	51.3	316	2	Q8CI22	Q8ci22 mus musculu
8	983	51.0	316	2	Q6AY99	Q6ay99 rattus norv
9	965	50.1	315	1	ALD1_MOUSE	P21300 mus musculu
10	961	49.8	303	2	Q68EJ1	Q68ej1 rattus norv
11	938	48.7	316	2	Q9QZI2	Q9qzi2 rattus norv
12	898	46.6	315	1	ALDR_RABIT	P15122 oryctolagus
13	884	45.9	315	1	ALDR_RAT	P07943 rattus norv
14	877	45.5	315	1	ALDR_MOUSE	P45376 mus musculu
15	876	45.4	315	1	ALDR_HUMAN	P15121 homo sapien
16	875	45.4	316	2	Q6FGA4	Q6fga4 homo sapien
17	873	45.3	315	1	ALDR_BOVIN	P16116 bos taurus
18	871	45.2	315	1	ALDR_PIG	P80276 sus scrofa
19	870	45.1	316	2	Q6ICP2	Q6icp2 homo sapien
20	859	44.6	317	2	Q90W83	Q90w83 gallus gall
21	839	43.5	327	2	Q6AZC3	Q6azc3 brachydanio
22	812	42.1	318	2	Q6PAB5	Q6pab5 xenopus lae
23	801	41.5	315	2	Q6IQU1	Q6iqu1 brachydanio
24	729.5	37.8	319	2	Q9DDC7	Q9ddc7 lepidodacty
25	659	34.2	316	2	Q9VTK9	Q9vtk9 drosophila
26	654.5	33.9	350	2	Q8IQF8	Q8iqf8 drosophila
27	623	32.3	301	1	AKE1_MOUSE	Q9dct1 mus musculu
28	623	32.3	324	2	Q6AZW2	Q6azw2 brachydanio
29	607.5	31.5	320	2	Q96JD6	Q96jd6 homo sapien
30	603	31.3	327	2	Q6GMC7	Q6gmc7 xenopus lae
31	593	30.8	325	2	Q8VCX1	Q8vcx1 mus musculu
32	586.5	30.4	326	1	AKD1_HUMAN	P51857 homo sapien
33	582.5	30.2	307	2	Q9BU71	Q9bu71 homo sapien
34	582.5	30.2	326	2	Q9TV64	Q9tv64 oryctolagus
35	581.5	30.2	335	2	Q7PCV3	Q7pcv3 anopheles g
36	577	29.9	292	2	Q7PF06	Q7pf06 anopheles g
37	576	29.9	324	1	AKA1_MOUSE	Q9jii6 mus musculu
38	572	29.7	325	2	Q80XJ7	Q80xj7 mus musculu
39	571	29.6	324	1	AKA1_RAT	P51635 rattus norv
40	564.5	29.3	326	1	AKD1_RAT	P31210 rattus norv
41	560	29.0	324	1	AKA1_HUMAN	P14550 homo sapien
42	555	28.8	333	2	Q6DKM7	Q6dkm7 xenopus lae
43	554	28.7	323	1	PE2R_RABIT	P80508 oryctolagus
44	550.5	28.6	304	2	Q6P702	Q6p702 xenopus lae
45	546	28.3	324	1	AKA1_PIG	P50578 sus scrofa

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2005, 19:48:55 ; Search time 5146 Seconds
                                           (without alignments)
                                           10263.542 Million cell updates/sec

Title: US-10-653-681A-1
Perfect score: 1090
Sequence: 1 caaaaacagcaacagaaagc..........ataaaaaaaataataatcat 1090

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                1: gb_ba:*
                2: gb_htg:*
                3: gb_in:*
                4: gb_om:*
                5: gb_ov:*
                6: gb_pat:*
                7: gb_ph:*
                8: gb_pl:*
                9: gb_pr:*
                10: gb_ro:*
                11: gb_sts:*
                12: gb_sy:*
                13: gb_un:*
                14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                 SUMMARIES
                        %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
     1   833   76.4   1337 9   HSU37100   U37100 Homo sapien
     2   830.8   76.2   1336 6   CQ718316   CQ718316 Sequence

	3	828.2	76.0	1551	9	BC008837	BC008837 Homo sapi
	4	828.2	76.0	1560	6	CQ776685	CQ776685 Sequence
	5	820.2	75.2	1611	9	AF524864	AF524864 Homo sapi
	6	796.6	73.1	1316	6	AR272611	AR272611 Sequence
	7	796.6	73.1	1316	6	AR276192	AR276192 Sequence
	8	796.6	73.1	1316	6	AR406467	AR406467 Sequence
	9	796.6	73.1	1316	6	AR440317	AR440317 Sequence
	10	796.6	73.1	1316	6	AR472475	AR472475 Sequence
	11	796.6	73.1	1316	6	AR543128	AR543128 Sequence
	12	796.6	73.1	1316	6	AX062696	AX062696 Sequence
	13	796.6	73.1	1316	6	AX367613	AX367613 Sequence
	14	796.6	73.1	1316	9	AF052577	AF052577 Homo sapi
	15	718	65.9	1315	6	AX743782	AX743782 Sequence
	16	651.8	59.8	3994	9	AL669847	AL669847 Human DNA
	17	651.8	59.8	121210	9	AL607022	AL607022 Human DNA
	18	574	52.7	574	9	AF044961	AF044961 Homo sapi
	19	508	46.6	1080	6	AX772965	AX772965 Sequence
	20	459.4	42.1	951	9	BT006794	BT006794 Homo sapi
	21	459.4	42.1	951	12	BT007750	BT007750 Synthetic
	22	458.4	42.1	948	9	CR541801	CR541801 Homo sapi
	23	431	39.5	951	6	AX380448	AX380448 Sequence
	24	431	39.5	951	6	AX772962	AX772962 Sequence
	25	395.6	36.3	473	9	AY347931	AY347931 Macaca ra
	26	377.8	34.7	144234	2	AP002425	AP002425 Homo sapi
c	27	377.8	34.7	144279	2	AP001570	AP001570 Homo sapi
c	28	377.8	34.7	216972	9	AC067819	AC067819 Homo sapi
	29	374.8	34.4	585	6	CQ732993	CQ732993 Sequence
c	30	361	33.1	137557	9	AC005909	AC005909 Homo sapi
	31	360.4	33.1	364	6	AX247463	AX247463 Sequence
	32	358.4	32.9	163631	9	AC009276	AC009276 Homo sapi
c	33	358.4	32.9	170919	9	AC078847	AC078847 Homo sapi
c	34	358.4	32.9	177373	2	AP002452	AP002452 Homo sapi
	35	358.4	32.9	196039	2	AC055757	AC055757 Homo sapi
	36	357.2	32.8	1268	10	CGU81045	U81045 Cricetulus
	37	354.4	32.5	1400	10	BC037690	BC037690 Mus muscu
	38	353.4	32.4	356	6	AX247461	AX247461 Sequence
	39	353.4	32.4	1446	10	BC079133	BC079133 Rattus no
	40	344.6	31.6	1413	10	AF182168	AF182168 Rattus no
	41	332	30.5	1315	10	BC005789	BC005789 Mus muscu
	42	331.6	30.4	1304	10	MMU04204	U04204 Mus musculu
	43	327.2	30.0	1225	6	CQ777549	CQ777549 Sequence
	44	327.2	30.0	1225	10	MUSMVDP	J05663 Mouse vas d
	45	327	30.0	993	10	RNO277957	AJ277957 Rattus no

Job time : 5184 secs

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2005, 19:42:42 ; Search time 701 Seconds
                                            (without alignments)
                                            9204.733 Million cell updates/sec

Title: US-10-653-681A-1
Perfect score: 1090
Sequence: 1 caaaaacagcaacagaaagc..........ataaaaaaaataataatcat 1090

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
                1: geneseqn1980s:*
                2: geneseqn1990s:*
                3: geneseqn2000s:*
                4: geneseqn2001as:*
                5: geneseqn2001bs:*
                6: geneseqn2002as:*
                7: geneseqn2002bs:*
                8: geneseqn2003as:*
                9: geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004as:*
                13: geneseqn2004bs:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
     1   833   76.4   1337 5   AAS68608   Aas68608 DNA encod
     2   833   76.4   1337 10   ADD71032   Add71032 Human ald
     3   832.2   76.3   1508 3   AAC98140   Aac98140 Human col
     4   828.2   76.0   1560 12   ADJ75119   Adj75119 Marker ge
     5   828.2   76.0   1560 12   ADN04246   Adn04246 Antipsori
     6   828.2   76.0   1560 13   ACN38728   Acn38728 Tumour-as
     7   828.2   76.0   1560 13   ADS85007   Ads85007 Human ato
     8   822.8   75.5   1549 12   ADK70274   Adk70274 Respirato
     9   796.6   73.1   1316 5   AAF68405   Aaf68405 Human lun
    10   796.6   73.1   1316 6   ABK38316   Abk38316 cDNA enco

                                Page 1

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    11   796.6   73.1   1316    7   ADS73134        Ads73134 Human kid
    12   796.6   73.1   1316    8   ACA10645        Aca10645 Human lun
    13   796.6   73.1   1316    8   ABX99596        Abx99596 Lung canc
    14   796.6   73.1   1316   10   ADH45842        Adh45842 Human lun
    15   796.6   73.1   1316   12   ADE72379        Ade72379 Human lun
    16   796.6   73.1   1316   13   ADJ19761        Adj19761 Human lun
    17   770.8   70.7   1621   12   ADH13722        Adh13722 Human ENZ
    18    718    65.9   1315   10   ADC97771        Adc97771 Human ARL
    19   635.4   58.3   1816   11   ACN92921        Acn92921 Breast ca
    20    616    56.5    770   13   ADR98739        Adr98739 Lung spec
    21   540.2   49.6   1170   12   ADH45334        Adh45334 Human enz
    22    508    46.6   1080    9   ACC83986        Acc83986 Human ald
c   23   439.8   40.3    558   10   ABZ84625        Abz84625 Toxicolog
    24    432    39.6    971   10   ADC10183        Adc10183 Human NOV
    25    431    39.5    951    6   ABA94733        Aba94733 Human dru
    26    431    39.5    966   10   ADC10185        Adc10185 Human NOV
    27   360.4   33.1    364    4   AAS39335        Aas39335 Novel hum
    28   353.4   32.4    356    4   AAS39333        Aas39333 Novel hum
    29   333.8   30.6   1926    5   AAS72230        Aas72230 DNA encod
    30   333.8   30.6   1926    5   AAS92672        Aas92672 DNA encod
    31   333.8   30.6   3620    5   AAS69995        Aas69995 DNA encod
    32   327.2   30.0   1225   12   ADJ75983        Adj75983 Marker ge
    33    317    29.1    540   12   ADP28822        Adp28822 Human sec
    34    316    29.0    585    2   AAZ24592        Aaz24592 Human lun
    35    316    29.0    585    3   AAC65831        Aac65831 Human lun
    36    316    29.0    585    6   ABL49050        Abl49050 Human lun
    37    316    29.0    585    6   ABQ92236        Abq92236 Human lun
    38    316    29.0    585    9   ADA28651        Ada28651 Human lun
    39    316    29.0    585   10   ADE53611        Ade53611 Human lun
    40    316    29.0    585   10   ADH36746        Adh36746 Human lun
    41    316    29.0    585   12   ADM56549        Adm56549 Human lun
    42    316    29.0    585   12   ADN89593        Adn89593 Human lun
c   43    316    29.0    857    9   ADA28650        Ada28650 Human lun
c   44    316    29.0    858    2   AAZ24591        Aaz24591 Human lun
c   45    316    29.0    858    3   AAC65830        Aac65830 Human lun
```

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2005, 22:13:45 ; Search time 228 Seconds
                                          (without alignments)
                                          7822.551 Million cell updates/sec

Title: US-10-653-681A-1
Perfect score: 1090
Sequence: 1 caaaaacagcaacagaaagc..........ataaaaaaaataataatcat 1090

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
               1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
               2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
               3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
               4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
               5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
               6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	828.2	76.0	1515	4	US-09-949-016-1344	Sequence 1344, Ap
2	796.6	73.1	1316	4	US-09-702-705-323	Sequence 323, App
3	796.6	73.1	1316	4	US-09-736-457-323	Sequence 323, App
4	796.6	73.1	1316	4	US-09-614-124B-323	Sequence 323, App
5	796.6	73.1	1316	4	US-09-671-325-323	Sequence 323, App
6	796.6	73.1	1316	4	US-09-589-184-323	Sequence 323, App
7	796.6	73.1	1316	4	US-09-658-824-323	Sequence 323, App
8	389.2	35.7	914	4	US-09-949-016-3127	Sequence 3127, Ap
9	358.4	32.9	17740	4	US-09-949-016-13086	Sequence 13086, A
10	328.6	30.1	601	4	US-09-949-016-46452	Sequence 46452, A
11	316	29.0	585	3	US-09-123-912-92	Sequence 92, Appl
12	316	29.0	585	3	US-09-643-597-92	Sequence 92, Appl
13	316	29.0	585	4	US-09-480-884A-92	Sequence 92, Appl
14	316	29.0	585	4	US-09-542-615A-92	Sequence 92, Appl
15	316	29.0	585	4	US-09-606-421B-92	Sequence 92, Appl
16	316	29.0	585	4	US-09-221-107-92	Sequence 92, Appl
17	316	29.0	585	4	US-09-466-396A-92	Sequence 92, Appl

	18	316	29.0	585	4	US-09-476-496A-92	Sequence 92, Appl
	19	316	29.0	585	4	US-09-630-940B-92	Sequence 92, Appl
	20	316	29.0	585	4	US-09-285-479-92	Sequence 92, Appl
c	21	316	29.0	858	3	US-09-123-912-91	Sequence 91, Appl
c	22	316	29.0	858	3	US-09-643-597-91	Sequence 91, Appl
c	23	316	29.0	858	4	US-09-480-884A-91	Sequence 91, Appl
c	24	316	29.0	858	4	US-09-542-615A-91	Sequence 91, Appl
c	25	316	29.0	858	4	US-09-606-421B-91	Sequence 91, Appl
c	26	316	29.0	858	4	US-09-221-107-91	Sequence 91, Appl
c	27	316	29.0	858	4	US-09-466-396A-91	Sequence 91, Appl
c	28	316	29.0	858	4	US-09-476-496A-91	Sequence 91, Appl
c	29	316	29.0	858	4	US-09-630-940B-91	Sequence 91, Appl
c	30	316	29.0	858	4	US-09-285-479-91	Sequence 91, Appl
	31	304.8	28.0	1335	4	US-09-023-655-1010	Sequence 1010, Ap
	32	292	26.8	1337	3	US-08-801-344-3	Sequence 3, Appli
	33	292	26.8	1337	3	US-09-498-599-3	Sequence 3, Appli
	34	288.4	26.5	601	4	US-09-949-016-46451	Sequence 46451, A
	35	170.2	15.6	1290	4	US-09-270-767-13724	Sequence 13724, A
	36	169.8	15.6	15141	4	US-09-949-016-14869	Sequence 14869, A
	37	165.4	15.2	601	4	US-09-949-016-46442	Sequence 46442, A
	38	165.4	15.2	601	4	US-09-949-016-113475	Sequence 113475,
	39	145.4	13.3	233	4	US-09-702-705-31	Sequence 31, Appl
	40	145.4	13.3	233	4	US-09-736-457-31	Sequence 31, Appl
	41	145.4	13.3	233	4	US-09-614-124B-31	Sequence 31, Appl
	42	145.4	13.3	233	4	US-09-671-325-31	Sequence 31, Appl
	43	145.4	13.3	233	4	US-09-589-184-31	Sequence 31, Appl
	44	145.4	13.3	233	4	US-09-658-824-31	Sequence 31, Appl
	45	141.6	13.0	292	4	US-09-313-294A-6562	Sequence 6562, Ap

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OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 00:12:25 ; Search time 748 seconds
                                            (without alignments)
                                            8675.151 Million cell updates/sec

Title: US-10-653-681A-1
Perfect score: 1090
Sequence: 1 caaaaacagcaacagaaagc..........ataaaaaaaataataatcat 1090

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5544816 seqs, 2976611598 residues

Total number of hits satisfying chosen parameters: 11089632

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
  No.   Score   Match Length DB ID   Description
----
     1   1090   100.0   1090 19 US-10-653-681A-1   Sequence 1, Appli

	2	832.2	76.3	1508	9	US-09-925-299-150	Sequence 150, App
	3	832.2	76.3	1508	10	US-09-925-299-150	Sequence 150, App
	4	796.6	73.1	1316	9	US-09-736-457-323	Sequence 323, App
	5	796.6	73.1	1316	9	US-09-902-941-323	Sequence 323, App
	6	796.6	73.1	1316	9	US-09-849-626-323	Sequence 323, App
	7	796.6	73.1	1316	10	US-09-476-300-323	Sequence 323, App
	8	796.6	73.1	1316	14	US-10-017-754-323	Sequence 323, App
	9	796.6	73.1	1316	15	US-10-102-524-1731	Sequence 1731, Ap
	10	796.6	73.1	1316	16	US-10-113-872-323	Sequence 323, App
	11	796.6	73.1	1316	17	US-10-283-017-323	Sequence 323, App
	12	718	65.9	1315	15	US-10-274-375-1	Sequence 1, Appli
	13	707	64.9	1279	19	US-10-653-681A-3	Sequence 3, Appli
	14	635.4	58.3	1816	14	US-10-198-846-14071	Sequence 14071, A
	15	431	39.5	951	15	US-10-274-694-36	Sequence 36, Appl
	16	431	39.5	951	18	US-10-332-448-36	Sequence 36, Appl
	17	360.4	33.1	364	10	US-09-803-719-2393	Sequence 2393, Ap
	18	353.4	32.4	356	10	US-09-803-719-2391	Sequence 2391, Ap
	19	316	29.0	585	9	US-09-735-705-92	Sequence 92, Appl
	20	316	29.0	585	9	US-09-850-716A-92	Sequence 92, Appl
	21	316	29.0	585	9	US-09-897-778-92	Sequence 92, Appl
	22	316	29.0	585	10	US-09-466-396A-92	Sequence 92, Appl
	23	316	29.0	585	14	US-10-007-700-92	Sequence 92, Appl
	24	316	29.0	585	15	US-10-117-982-92	Sequence 92, Appl
	25	316	29.0	585	17	US-10-313-986-92	Sequence 92, Appl
	26	316	29.0	585	18	US-10-775-972-92	Sequence 92, Appl
c	27	316	29.0	858	9	US-09-735-705-91	Sequence 91, Appl
c	28	316	29.0	858	9	US-09-850-716A-91	Sequence 91, Appl
c	29	316	29.0	858	9	US-09-897-778-91	Sequence 91, Appl
c	30	316	29.0	858	10	US-09-466-396A-91	Sequence 91, Appl
c	31	316	29.0	858	14	US-10-007-700-91	Sequence 91, Appl
c	32	316	29.0	858	15	US-10-117-982-91	Sequence 91, Appl
c	33	316	29.0	858	17	US-10-313-986-91	Sequence 91, Appl
c	34	316	29.0	858	18	US-10-775-972-91	Sequence 91, Appl
	35	304.8	28.0	1331	18	US-10-737-450-97	Sequence 97, Appl
	36	304.8	28.0	1335	17	US-10-641-643-1010	Sequence 1010, Ap
	37	304.8	28.0	1367	9	US-09-864-864-332	Sequence 332, App
	38	304.8	28.0	1367	15	US-10-171-581-1	Sequence 1, Appli
	39	304.8	28.0	1367	17	US-10-172-118-641	Sequence 641, App
	40	304.8	28.0	1367	17	US-10-342-887-641	Sequence 641, App
	41	304.8	28.0	1367	18	US-10-717-597-289	Sequence 289, App
	42	304.8	28.0	1368	18	US-10-416-330-21	Sequence 21, Appl
	43	292	26.8	1337	17	US-10-205-331-29	Sequence 29, Appl
	44	292	26.8	1339	17	US-10-191-803-12	Sequence 12, Appl
	45	292	26.8	1339	17	US-10-152-319A-1492	Sequence 1492, Ap

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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 18, 2005, 23:59:48 ; Search time 182.5 Seconds
                                            (without alignments)
                                            4619.932 Million cell updates/sec

Title: US-10-653-681A-1
Perfect score: 1928
Sequence: 1 caaaaacagcaacagaaagc..........ataaaaaaaataataatcat 1090

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10653681/runat_18032005_171050_1272/app_query.fasta_1.
1287
-DB=A_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10653681_@CGN_1_1_224_@runat_18032005_171050_1272 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   A_Geneseq_16Dec04:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*

     Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1274	66.1	339	4	ABG04421	Abg04421 Novel hum
2	1268	65.8	358	3	AAB53383	Aab53383 Human col
3	1159	60.1	316	3	AAB10872	Aab10872 Human ARL
4	1159	60.1	316	7	ABR62325	Abr62325 Human ald
5	1159	60.1	316	7	ADC97773	Adc97773 Human ARL
6	1159	60.1	316	8	ADK70537	Adk70537 Respirato
7	1159	60.1	316	8	ADJ75577	Adj75577 Marker ge
8	1159	60.1	316	8	ADN04247	Adn04247 Antipsori
9	1159	60.1	316	8	ABM80941	Abm80941 Tumour-as
10	1159	60.1	316	8	ADS85008	Ads85008 Human ato
11	1154	59.9	316	4	AAB76864	Aab76864 Human lun
12	1154	59.9	316	5	AAU85519	Aau85519 Clone #18
13	1154	59.9	316	6	ABU69491	Abu69491 Human lun
14	1154	59.9	316	6	ABU66393	Abu66393 Lung canc
15	1154	59.9	316	7	ADH45859	Adh45859 Human lun
16	1154	59.9	316	8	ADE71611	Ade71611 Human lun
17	1154	59.9	316	8	ADJ19778	Adj19778 Human lun
18	1084.5	56.2	293	8	ADH45296	Adh45296 Human enz
19	1073	55.7	316	7	ADC97772	Adc97772 Human ARL
20	1058	54.9	316	5	ABB07530	Abb07530 Human dru
21	1058	54.9	316	7	ABR62324	Abr62324 Human ald
22	1058	54.9	316	7	ADC10186	Adc10186 Human NOV
23	1056	54.8	316	7	ADC10184	Adc10184 Human NOV
24	961	49.8	316	3	AAB10871	Aab10871 Murine MV
25	961	49.8	316	8	ADJ76302	Adj76302 Marker ge
26	920	47.7	287	8	ADH13653	Adh13653 Human ENZ
27	889	46.1	316	2	AAW69357	Aaw69357 Rat lens
28	889	46.1	316	6	ABM04798	Abm04798 Rat aldos
29	884	45.9	315	7	ADE57875	Ade57875 Rat Prote
30	884	45.9	315	7	ADE57879	Ade57879 Rat Prote
31	884	45.9	315	7	ADE57883	Ade57883 Rat Prote
32	884	45.9	315	7	ADE57887	Ade57887 Rat Prote
33	884	45.9	315	7	ADE57867	Ade57867 Rat Prote
34	884	45.9	315	7	ADE57871	Ade57871 Rat Prote
35	882	45.7	316	8	ADS85097	Ads85097 Mouse ato
36	882	45.7	328	4	ABG11687	Abg11687 Novel hum
37	879	45.6	316	5	ABB83356	Abb83356 Murine TS
38	878	45.5	316	2	AAR15425	Aar15425 Human ald
39	876	45.4	315	7	ADE57869	Ade57869 Human Pro
40	876	45.4	315	7	ADE57877	Ade57877 Human Pro
41	876	45.4	315	7	ADE57885	Ade57885 Human Pro
42	876	45.4	315	7	ADE57881	Ade57881 Human Pro
43	876	45.4	315	7	ADE57889	Ade57889 Human Pro
44	876	45.4	315	7	ADE57873	Ade57873 Human Pro
45	876	45.4	315	8	ADP90915	Adp90915 Human ald